

Extended abstract**Anaerobic chytrids from herbivores**AJP Trinci¹, G Mennim¹, JL Brookman^{1,2}, MK Theodorou²

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Extant eukaryotic anaerobes such as the anaerobic chytrids are either precambrian relicts which have survived in residual anaerobic environments, or (and this is most likely) anaerobes which have evolved secondarily from aerobic eukaryotes. Importantly, both anaerobic and aerobic chytrids have cell walls containing chitin and have very similar morphologies and life cycles [1]. Furthermore, analysis of 18S rRNA sequence data [2-4] suggests that both belong to the class Chytridiomycetes, the first group to diverge from the major fungal evolutionary line some 470Ma ago [5]; they probably diverged at about the time when the first land plants appeared (ca. 400Ma ago). The acquisition of hydrogenosomes by anaerobic chytrids represents a landmark event in this divergence; hydrogenosomes are organelles bounded by a single or double membrane which lack DNA and cytochromes but contain the enzymes pyruvate:ferredoxin oxidoreductase and hydrogenase. Current opinion supports the view that hydrogenosomes evolved independently from mitochondria within several protist lineages

(they occur in trichomonads and ciliates as well as in anaerobic chytrids) but it is not known how these organelles acquired pyruvate : ferredoxin oxidoreductase and hydrogenase [6]. Thus, considering the origin of anaerobic chytrids, the timing of the acquisition of hydrogenosomes is a very important event. The organelle either evolved in free-living chytrids colonising terrestrial or aquatic anaerobic environments or in chytrids following the early invasion of the digestive tract of proto-ungulates (the common ancestor) or following a later invasion of the digestive tract of perissodactyls (horse, rhinoceros and tapir) and/or artiodactyls (pig, hippopotamus, camel, deer, giraffe, cattle and sheep). Importantly, analysis of 18S rRNA [2] and ITS1 [7] sequence data shows that anaerobic chytrids are monophyletic (i.e. they had a single ancestor which was either the ancestral, free-living anaerobic chytrid or the ancestral, free-living aerobic chytrid which invaded the digestive tract of herbivores). In either event, the lack of host specificity [8-10] would be sufficient to explain the present day ubiquitous dis

tribution of anaerobic chytrids in herbivorous animals.

Apart from the hydrogenosomes, features of anaerobic chytrids of particular biological interest include the polyflagellate zoospores of some species, the low G+C content (13 to 22%) of the DNA of all species [11,12] and the possible horizontal transfer of DNA to anaerobic chytrids from other microorganisms present in the digestive tract of herbivores. Exploitation of anaerobic chytrids has focused on their potential for increasing the digestibility of high fibre lignocellulose diets of domestic animals and on the use of their enzymes (following transfer to a suitable host for production purposes) for industrial applications (e.g. the pulp bleaching formulation, Ecozyme™ contains a genetically modified xylanase from *Neocallimastix patriciarum*). As far as future exploitation of anaerobic chytrids is concerned, it will be important to establish the diversity of the group and to assess the extent to which incultured species remain to be isolated.

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